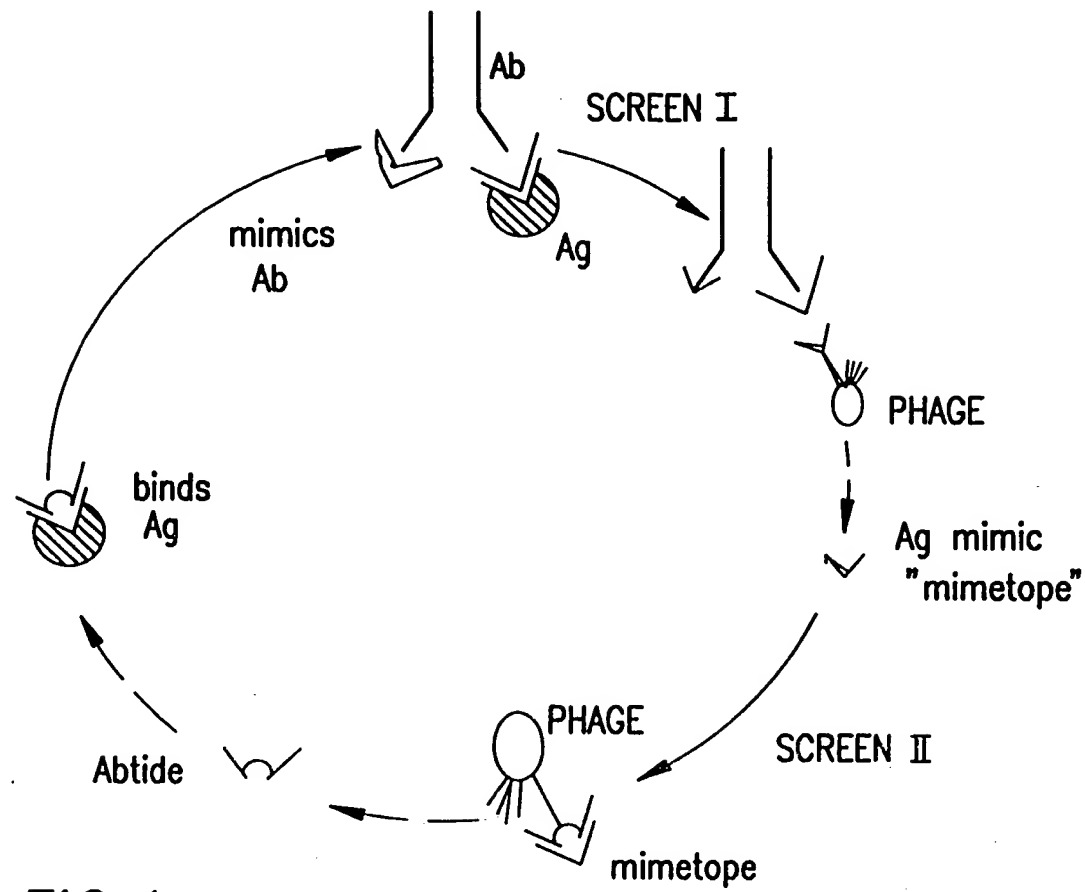

FIG.1

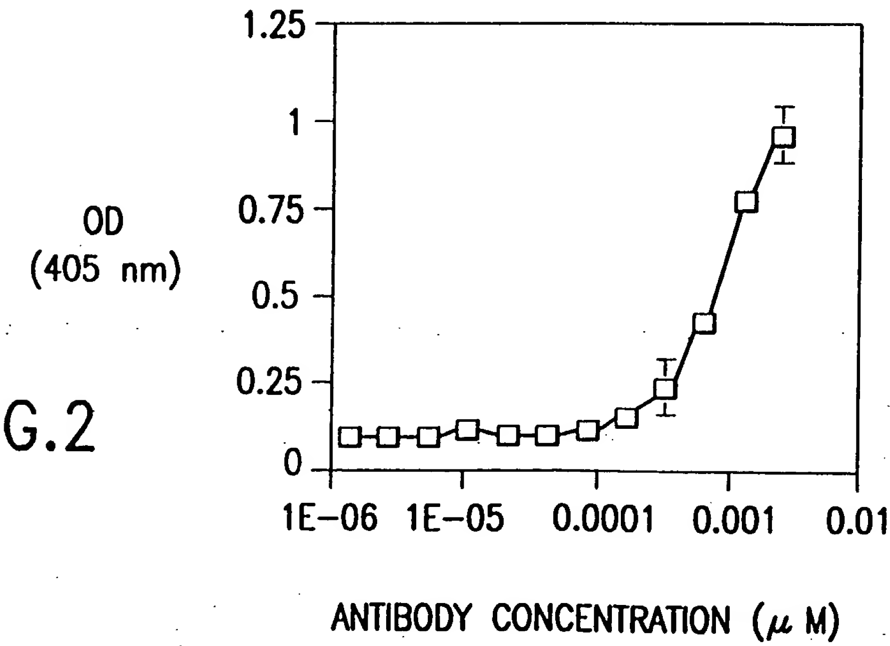

FIG.2

CLONE 14

GIINANDPLPFWFMS--PYTPGPAPIDINASRALVS-NESG
WQGTHFPYT LVSKNDSG
CDR3L CDR2L
(5/9 = 55.5 %) (7/8 = 87.5 %)

CLONE 17

DL-SRNLDFGRFLLYNA--YVPGFTPTFISLTAEHLSSPKG
LVSKN-DSG WQGTHF-P-YT
CDR2L CDR3L
(6/8 = 75 %) (6/9 = 66.6 %)

CLONE 15

CGRAYCL-SGNYNIFGALFPGVS--TPYADVGHDDAQSWRR
LVSKN-DS-G WQG-THFPYT
CDR2L CDR3L
(4/8 = 50 %) (6/9 = 66.6 %)

CLONE 13

RCSPIW-GIS-YPFGLLSSNPGVCHSSDAET-NIRNDILTT
WQG-THFPYT GSDN-K-SVL
CDR3L CDR2L(REV)
(6/9 = 66.6 %) (4/8 = 50 %)

CLONE 16

GHSNYCFVSTLGMPIVGFP-SINARGLIHYGGSDPR--LAA
WQGTHFPYT GSDNKSVL
CDR3L CDR2L(REV)
(3/9 = 33.3 %) (5/8 = 62.5 %)

FIG.3

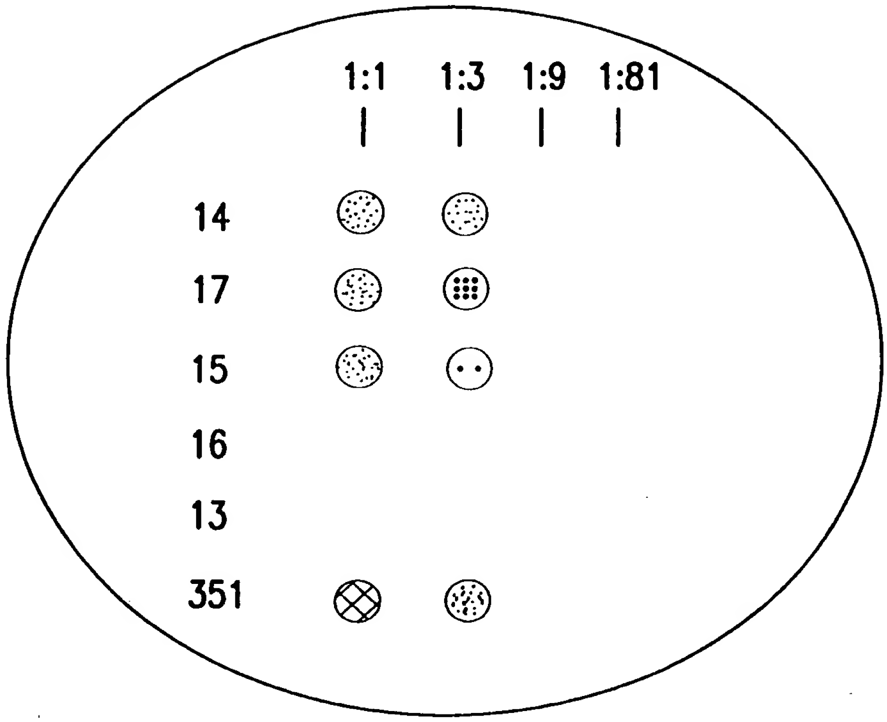

FIG.4

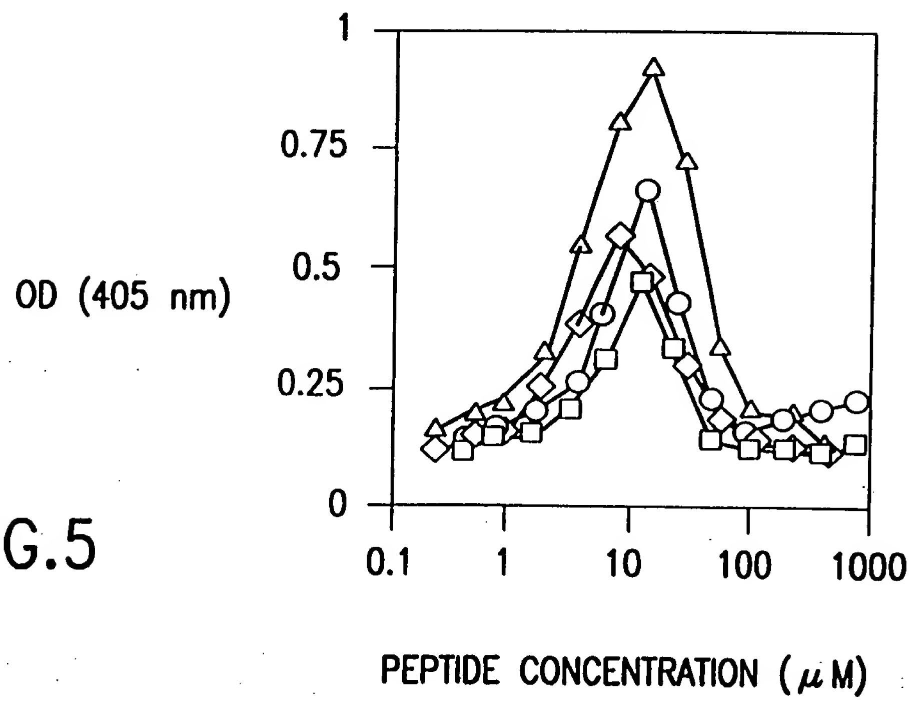

FIG.5

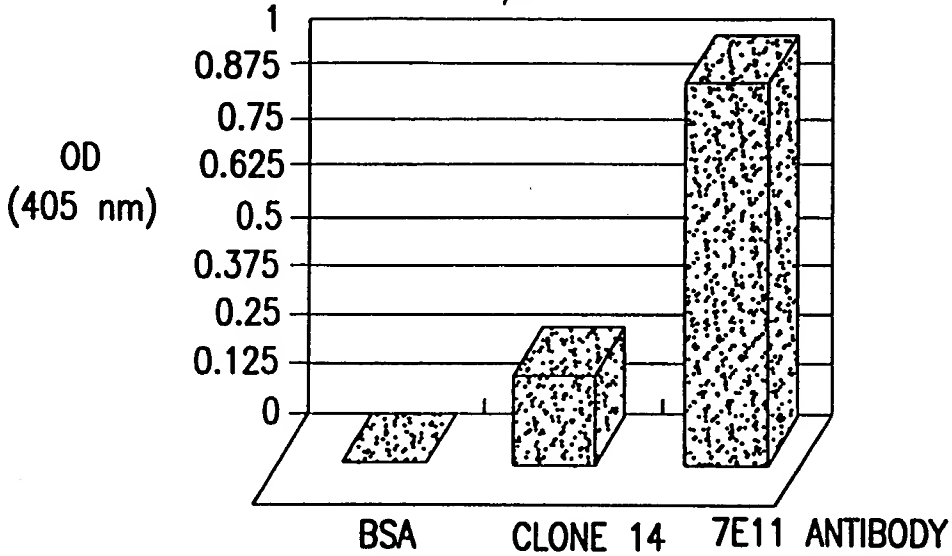

FIG.6

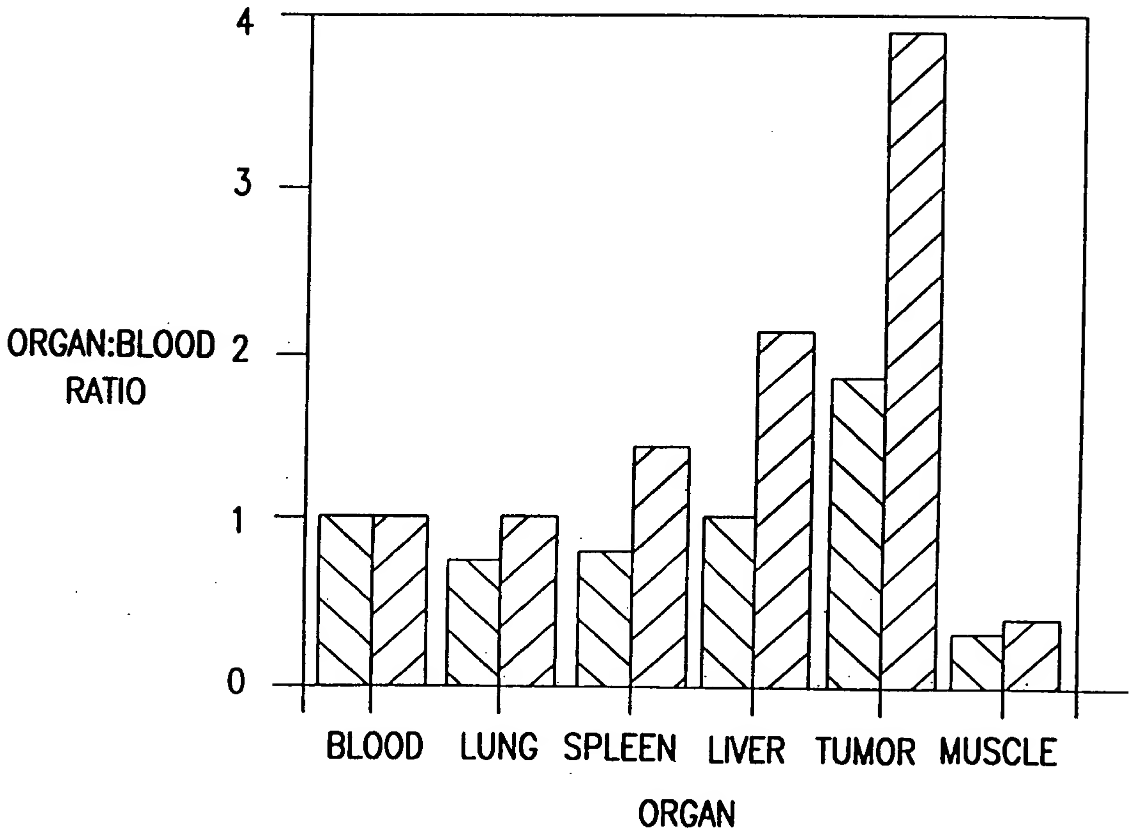

FIG.7

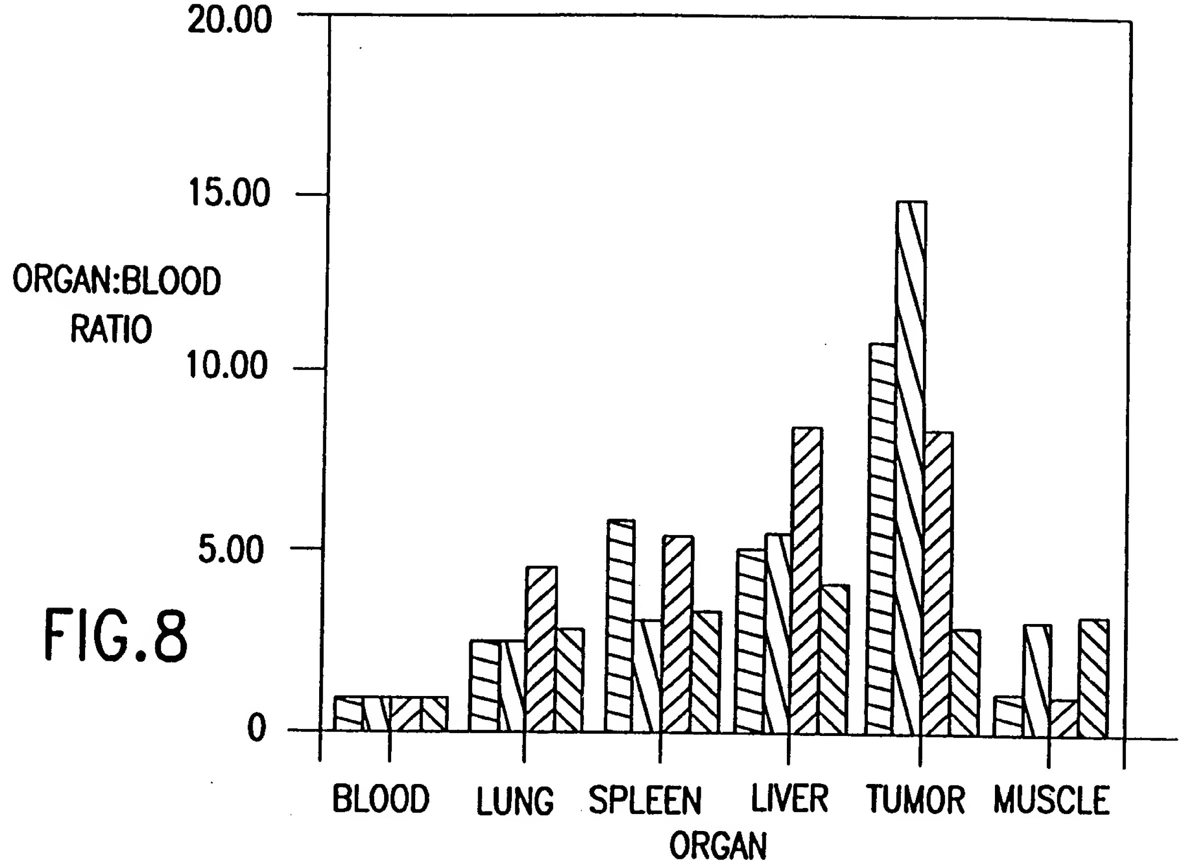

FIG.8

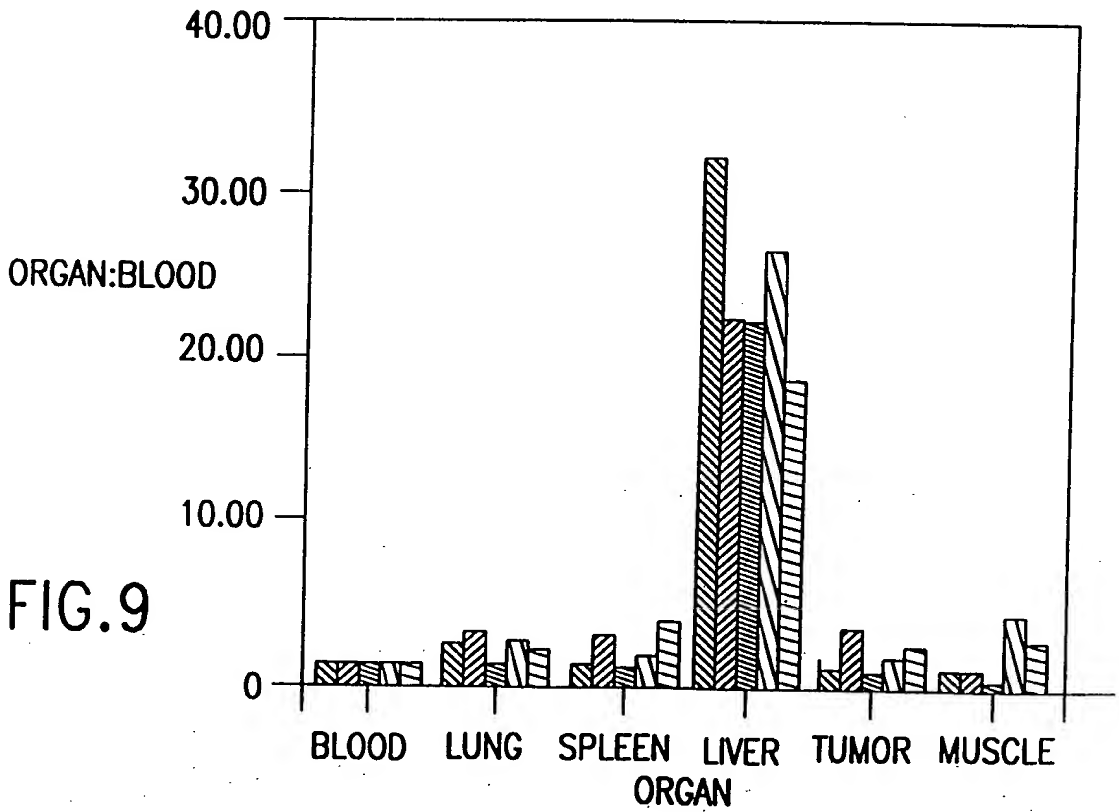

FIG.9

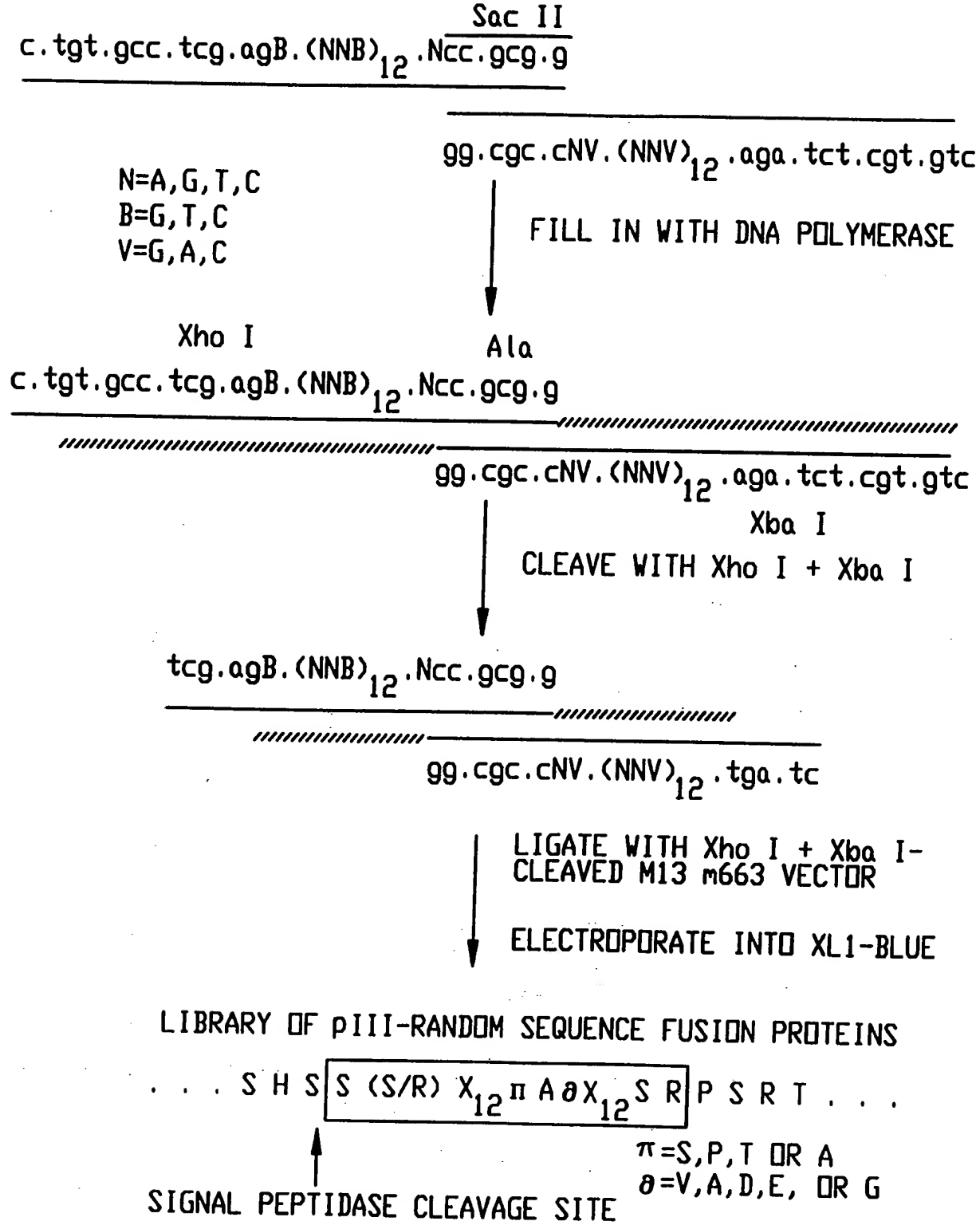

FIG.10

G TGT GTC TCG AGN $(NNB)_{20}$ NAC GCC AN

NTG CGG TNV $(NNV)_{15}$ AGA TCT GTG TTG

N=A,C,G,T
B=C,G,T
V=A,C,G

↓ FILL IN WITH SEQUENASE

Xho I

G TGT GTC TCG AGN $(NNB)_{20}$ NAC GCC AN

NTG CGG TNV $(NNV)_{15}$ AGA TCT GTG TTG
Xba I

↓ RESTRICT WITH Xho I AND Xba I

TCG AGN $(NNB)_{20}$ NAC GCC AN

NTG CGG TNV $(NNV)_{15}$ AGA TC

↓ LIGATE WITH Xho I + Xba I-CLEAVED M13mp18Xa

↓ ELECTROTRANSFORM E. coli JS5

D38 GENETIC DIVERSITY LIBRARY DISPLAYED AS RANDOM N-TERMINAL pIII FUSIONS

. . H S S (S/R) X_{20} (Y/H/N/D) A (I/M/T/N/K/S/R) X_{15} S R

↑ SIGNAL PEPTIDASE CLEAVAGE SITE

FIG.11

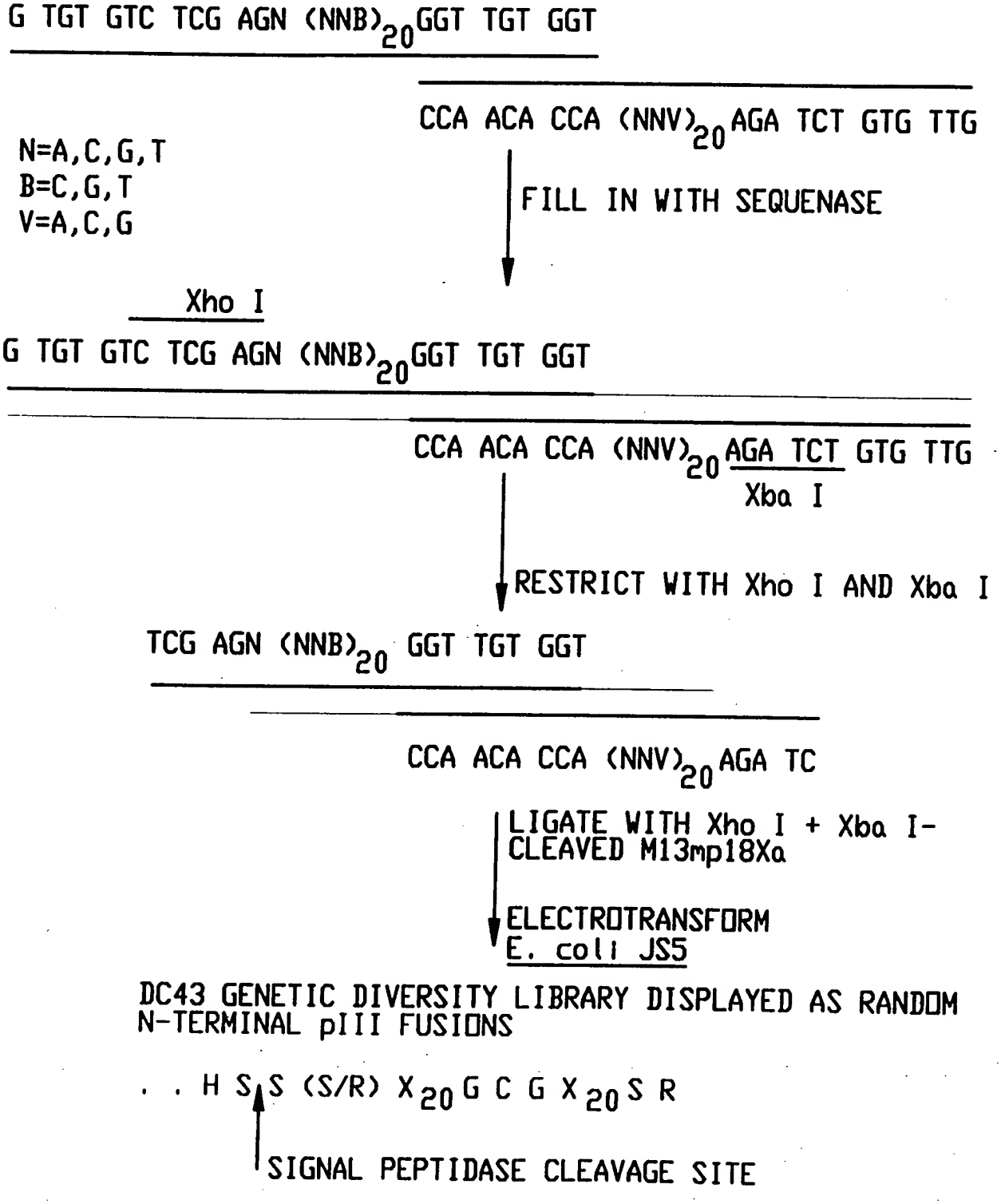

FIG.12

G A P V W R G N P R W R G P G G F K W P G C G N G P M C N T F T P A R G G S R N N G P

5' ggs-gcs-ccs-gts-tgs-ags-ggs-aas-ccs-cgs-tgs-ags-ggs-ccs-ggs-ggs-tts-aas-tgs-ccs-GGC-TGC-GGG 3'

MP-1 oligo 1

3' CCG-ACG-CCC-tts-ccs-ggs-tas-acs-tis-tgs-aas-tgs-ggs-cgs-gcs-ccs-ccs-ags-gcs-tts-tts-ccs-ggs 5'

MP-1 oligo 2

FIG.13